



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 139767

TO: James Schultz
Location: REM/2D18/2C18
Art Unit: 1635
Wednesday, December 08, 2004

Case Serial Number: 09/913800

From: David Schreiber
Location: Biotech-Chem Library
Remsen E01A61
Phone: 272-2526

david.schreiber@uspto.gov

Search Notes

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>P. Schreder</u>	NA Sequence (#) <u>22</u>	STN _____
Searcher Phone #: <u>272-2526</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>Ramsen E01A61</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>12/8</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep. Review Time <u>15</u>	Fulltext _____	Sequence Systems <u>Compuer</u>
Clerical Prep. Time: _____	Patent Family _____	WWW/Internet _____
Online Time <u>126</u>	Other _____	Other (specify) _____

Schreiber, David

139767

From: Schultz, James
Sent: Wednesday, November 17, 2004 10:09 AM
To: Schreiber, David
Subject: Score over length search 09/913,800

Hi David,

I need a score over length nucleotide sequence search on SEQ ID NOS: 32 and 21 in the above entitled case. I need the lower and upper limits to be 8 and 30, respectively, I only need hits that are 100% complementary, and please transfer as many hits into the excel program as possible. No need to search the interference databases at this time.

I realize you don't normally search more than two sequences, but applicants have asserted that these two sequences are usable together, and that they both comprise the invention...I don't see any way around searching these.

Also, can you give me an idea how long it is typically taking to get results back these days for this type of search?

Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 100⁷⁰.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

PT first, second and third zinc fingers, ordered from N- to C-terminus.
 PS Example 1, Page 63; 81pp; English.
 XX

CC The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsequence. Also described are: (i) a polypeptide
 CC (II) comprising (i); (2) a polynucleotide (III) encoding (i) or (ii); and
 CC (3) designing (iv) (1) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsequence, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsequence, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsequence, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsequences
 CC having the nucleotide G in the 5'-most position of the subsequence. (I) is
 CC useful in studying gene function, and for human therapeutic and plant
 CC engineering. (II), (III) or (IV) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention
 CC

XX Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
 XX

Query Match 50.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 4 GAGGCTGTT 12
 |||||
 1 GAGGCTGTT 9
 Db

RESULT 3
 ADA64507
 ID ADA64507 standard; DNA; 9 BP.
 XX
 AC ADA64507;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Zinc finger target sequence DNA #965.
 XX
 KW ds; target sequence; zinc finger protein; improved affinity;
 KW multi-finger zinc finger protein; improved specificity;
 KW improved specificity; enhanced biological activity.
 XX
 OS Synthetic.
 OS
 PN US2003068675-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 20-NOV-2001; 2001US-00990186.
 XX
 XX 24-MAR-1999; 99US-0126238P.
 PR 24-MAR-1999; 99US-0126238P.
 PR 30-JUL-1999; 99US-0146595P.
 PR 30-JUL-1999; 99US-0146595P.
 PR 23-MAR-2000; 2000US-00535008.
 PR 20-NOV-2000; 2000US-00716637.
 XX
 PA (LNUQ/) LNU Q.
 XX
 PI Liu Q;
 XX
 DR WPI; 2003-567233/53.
 XX

PT Designing zinc finger protein that has three zinc fingers from N-terminus
 PT and C-terminus that bind to substrates in 3' to 5' direction, in a target
 PT site, by selecting zinc fingers that bind their respective substrates.
 XX

PS Disclosure; Page 27; 34pp; English.
 XX

CC The invention relates to a method of designing a zinc finger protein. The
 CC method is useful for designing a zinc finger protein. The method provides
 CC multi-finger zinc finger proteins with improved affinity and specificity
 CC for their target sequences, as well as enhanced biological activity. The
 CC present sequence represents a zinc finger protein DNA target sequence.
 XX

XX Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
 XX

Query Match 50.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

QY 4 GAGGCTGTT 12
 |||||
 1 GAGGCTGTT 9
 Db

RESULT 4
 ADM23199
 ID ADM23199 standard; DNA; 9 BP.
 XX
 AC ADM23199;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Synthetic zinc finger protein target DNA #965.
 XX
 KW Zinc finger protein; triplet target subsequence; zinc finger motif; sp-1; ds.
 KW zinc finger protein; triplet target subsequence; zinc finger motif; sp-1; ds.
 XX
 OS Unidentified.
 OS
 PN US2003104526-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 20-NOV-2001; 2001US-00989994.
 XX
 PR 24-MAR-1999; 99US-0126238P.
 PR 24-MAR-1999; 99US-0126238P.
 PR 30-JUL-1999; 99US-0146595P.
 PR 30-JUL-1999; 99US-0146595P.
 PR 23-MAR-2000; 2000US-00535008.
 PR 20-NOV-2000; 2000US-00716637.
 XX
 PA (LNUQ/) LNU Q.
 XX
 PI Liu Q;
 XX
 DR WPI; 2003-843091/78.
 XX

PT New zinc finger protein used for recognizing triplet target substrates
 PT having nucleotide G in 5'-most position of subsequence, that has been
 PT optimized with respect to location of subsequence within target site.
 XX

PS Example 6; SEQ ID NO 2478; 48pp; English.
 XX

CC The invention describes a new zinc finger protein that binds to a target
 CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
 CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
 CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
 CC (S3) target subsequences. The zinc finger proteins can be used for
 CC recognising triplet target subsequences having the nucleotide G in the 5'-
 CC most position of the subsequence, that has been optimised with respect to the
 CC location of the subsequence within the target site. This sequence represents
 CC the target polynucleotide to which the zinc finger protein sp-1 consensus
 CC sequence binds.
 XX

SO Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GAGGCTGTT 12
 |||||
 1 GAGGCTGTT 9

RESULT 5

AAA80787
 ID AAA80787 standard; DNA; 8 BP.

AC AAA80787;

DT 24-NOV-2000 (first entry)

DE A. thaliana primer walking octamer SEQ ID NO: 100.

XX Primer walking; octamer; primer; DNA sequencing; PCR; ss.

XX Arabidopsis thaliana.

XX US6083695-A.

PD 04-JUL-2000.

PF 21-MAY-1997; 97US-00859954.

XX 15-APR-1996; 96US-00632782.

XX (UYHO-) UNIV HOUSTON.

PA (HARD/) HARDIN S H.

PI Hardin PE, Hardin SH, Homayouni R;
 WPI; 2000-474852/41.

XX Sequencing an unknown DNA molecule for the polymerase chain reaction and
 PT other primer processes comprises primer walking of octamer
 PT oligonucleotides.

PS Example 8; Col 75-76; 161pp; English.

XX This invention describes a novel method for sequencing an unknown DNA
 CC molecule which comprises selecting a library primer from an octamer
 CC oligonucleotide library consisting of 48 8-bp sequences and corresponding
 CC complementary sequences, where the library primer is complementary to a
 CC known sequence adjacent to the unknown sequence or is complementary to a
 CC sequence in a known extension product. The method is useful for DNA
 CC nucleotide sequencing, in PCR, and in other processes which make use of
 CC primers. The octamers are used to identify coding sequences. Primer
 CC walking using the octamer libraries is advantageous over other sequencing
 CC methods because it does not require multiple cloning steps nor subsequent
 CC template preparations, and it is a directed and methodical approach.
 CC AAA80688-A81253 represent the octamer primers used in the primer walking
 CC method of the invention

XX Sequence 8 BP; 1 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 44.4%; Score 8; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTGAGGCT 9
 |||||
 1 TTGAGGCT 8

Search completed: December 8, 2004, 06:35:34
 Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:38:09 ; Search time 0.001 Seconds
(without alignments)
0.972 Million cell updates/sec

Title: US-09-913-800-21

Perfect score: 18
Sequence: 1 cttgagctgtgtgagac 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 3 seqs, 27 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database: rnpb21.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	9	50.0	9	1	US-09-989-789-2478 Sequence 2478, Ap
2	9	50.0	9	1	US-09-990-186-2478 Sequence 2478, Ap
3	9	50.0	9	1	US-09-989-994-2478 Sequence 2478, Ap

ALIGNMENTS

RESULT 1
US-09-989-789-2478
; Sequence 2478, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTGTT 12
|||||
DB 1 GAGGCTGTT 9

RESULT 2

US-09-990-186-2478
; Sequence 2478, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTGTT 12
|||||
DB 1 GAGGCTGTT 9

RESULT 3

US-09-989-994-2478
; Sequence 2478, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGCTGTT 12
|||||
DB 1 GAGGCTGTT 9

Search completed: December 8, 2004, 06:38:10
Job time: 1 sec

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:41:41 ; Search time 0.001 Seconds
(without alignments)
0.360 Million cell updates/sec

Title: US-09-913-800-32

Perfect score: 18
Sequence: 1 GTGAGCGACTTCATCCTT 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 1 seqs, 10 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database: rge32.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	10	55.6	10	1	BD239875 ACCESSION:BD239875

ALIGNMENTS

RESULT 1
BD239875/c
LOCUS BD239875 10 bp DNA linear PAT 17-JUN-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239875
VERSION BD239875.1 GI:33049645
KEYWORDS JP 2002534056-A/1293.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
Robert, B.L. and Shankar, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1293 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1293
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878, 19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000, 19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044, 19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080, 19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994, 19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078, 19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1. .10 /organism='Homo sapiens (human)'.
FEATURES
source 1. .10 /organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 55.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
Db 10 TGAGCGACTT 1

Search completed: December 8, 2004, 06:41:41
Job time: 0.001 secs

PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.

XX (GEN2) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

DR WPI; 2000-106077/09.

PT Isolated polynucleotides differentially expressed in antigen-presenting
 cells, useful in gene vaccines against cancer.

PS Claim 1; Page 102; 130pp; English.

XX Sequences AA27573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells. Immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells

XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 55.6%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGAGGCACTT 11
 |||||

Db 10 TGAGGCACTT 1

Search completed: December 8, 2004, 06:43:02
 Job time : 0.001 secs

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Search completed: December 8, 2004, 06:44:34
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:44:34 ; Search time 0.001 Seconds
(without alignments)
0.648 Million cell updates/sec

Title: US-09-913-800-32

Perfect score: 18
Sequence: 1 GTGAGCGACTTCATCCTT 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 1 seqs, 18 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : rni32.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1	US-09-256-465-32 Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-256-465-32
; Sequence 32, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-465-32

Query Match 100.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGAGCGACTTCATCCTT 18
|||
Db 1 GTGAGCGACTTCATCCTT 18

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:45:59 ; Search time 0.001 Seconds
(without alignments)
0.360 Million cell updates/sec

Title: US-09-913-800-32

Perfect score: 18

Sequence: 1 gtagcgacttcacccct 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 10 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : rnpb32.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10	55.6	10	1	US-10-033-145-1293

ALIGNMENTS

RESULT 1
US-10-033-145-1293/C
; Sequence 1293, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1293
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1293

Query Match 55.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TGAGCGACTT 11

Db 10 TGAGCGACTT 1

Search completed: December 8, 2004, 06:46:00
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:36:40 ; Search time 0.001 Seconds
(without alignments)
0.936 Million cell updates/sec

Title: US-09-913-800-21

Perfect score: 18
Sequence: 1 cttgagcctgtggcgac 18

Scoring table: Identity_NUC
Gapop 10.0 ; Gapext 0.5

Searched: 2 seqs, 26 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 8

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2 summaries

Database : rn121.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	1	US-09-256-465-21
2	8	44.4	8	1	US-08-859-954-100

ALIGNMENTS

RESULT 1
US-09-256-465-21
Sequence 21, Application US/09256465
Patent No. 6043090
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
FILE REFERENCE: RTS-0035
CURRENT APPLICATION NUMBER: US/09/256,465
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 21
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-09-256-465-21

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGAGCCTGTGGCGAC 18
|||||

Db 1 CTTGAGCCTGTGGCGAC 18

RESULT 2

US-08-859-954-100
Sequence 100, Application US/08859954
Patent No. 6083695

GENERAL INFORMATION:

APPLICANT: Hardin, Susan H.

APPLICANT: Homayouni, Ramin

APPLICANT: Hardin, Paul E.

TITLE OF INVENTION: Design and Optimized Primer Library for

TITLE OF INVENTION: Gene Sequencing and Method Thereof

NUMBER OF SEQUENCES: 566

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 1301 McKinney, Suite 5100

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77010-1095

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/859,954

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/632,782

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Paul, Thomas D.

REGISTRATION NUMBER: 32,714

REFERENCE/DOCKET NUMBER: D-5900

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/651-5325

TELEFAX: 713/651-5246

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "oligonucleotide"

HYPOTHETICAL: YES

ANTI-SENSE: YES

US-08-859-954-100

Query Match 44.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGAGCCT 9
|||||
Db 1 TTGAGCCT 8

Search completed: December 8, 2004, 06:36:41
Job time : 1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:34:24 ; Search time 0.001 Seconds
(without alignments)
0.324 Million cell updates/sec

Title: US-09-913-800-21

Perfect score: 18
Sequence: 1 cttgagcgtgtgagcgcac 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 9 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rge21.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	9	50.0	9 1 AX669029	ACCESSION:AX669029

ALIGNMENTS

RESULT 1
AX669029
LOCUS AX669029 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2478 from Patent WO0242459.
ACCESSION AX669029
VERSION AX669029.1 GI:29292006
KEYWORDS
SOURCE .
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
JOURNAL Patent: WO 0242459-A 2478 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
source Location/Qualifiers
1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GAGGCTGTT 12
|||||||
Db 1 GAGGCTGTT 9

Search completed: December 8, 2004, 06:34:24
Job time : 0.001 secs